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PAT 10-APR-2003
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Homo sapiens sapiens
Bokaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini; Hominidae, Homo.
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L00.0%; Score 12; DB 6; Length 28;

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Matches 12; Conservative 0; Mismatches 0; Indels
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/organism='Unidentified'.
Location/Qualifiers
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AR257926.1 31:29698051
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Sequence 2 from Patent WO0118039.
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Contran, M.D. and Junker, D.E.
Recombinant swinepox virus
Recombinant swinepox virus
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/organish="unknown'
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BARBARA J WINSLOW,WARK D COCKRAN
C12N15/09, A61X9/12, A61X99/125, A61X39/15, A61X39/213,
A61X39/245,
A61X48/00, A61P43/00, C12N7/00//C07X14/705, C12N15/00 CC PIV
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Recombinant virus expressing foreign DNA encoding feline CD80, feline CTRA-4 or feline interferon-gamma and uses thereof.
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Minslow,B.J., and Cochran,M.D.
Renoshbant virus expressing foreign DNA encoding feline CD80,
feline CD86, feline CTLA-4 or feline interferon-gamma and uses
Schent. UP 2002513591-A 75 14-MAY-2002;
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S. Cochran, M. D. And Junker, D.E.
S. Cochran, M. D. And Junker, D.E.
S. Ascombinant Winepox virus
Patent: .US 6221361-A 84 24-APR-2001;
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Sequence 84 from patent US 6221361.
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AR147023.1 GI:15110826
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27 GGAAAGTAAAA 16
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	March 25, 2004, 08:39:03 ; Search time 6718.14 Seconds (without alignments) 6361.316 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-963-285-1_COPY_1250_2235 986 1 ctgccattccaatccagcgcgagccgtctcggaagcagca 985	
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched:	3470272 seqs, 21671516995 residues	
Total number of	Total number of hits satisfying chosen parameters: 6940544	
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	GenEmbl: • 1 gb ba: • 2: gb ba: •	

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ACO09108 168656 bp DNA linear PRI 29-OCT-2002
Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
ACO09108
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Dof Joint Genome Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOS Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Bob Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.

Submitted (29-OCT-2002) DOE Joint Genome Institute, 2800 Mitchell
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Submitted (29-CCT-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnur Creek, CA 94599 USA
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Quality: Phrap Quality >=40 99.9% of Sequence;
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Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos Mational Laboratory.
Unpublished
592 AACTITICCCAATCCCTAAAAGGACTIGGCCICTITITCTGGGCTCAGCGGGCAGCCG 751
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try, 1-1-1 Hondo, Akita 010, JAPAN
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gene="MFH-1"

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fordoutc = Wesenchyme Fork Head-1"

fordoutc = Wesenchyme Fork Head-1"

fordoutc = Wesenchyme Fork Head-1"

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db_xref="SMISS-PROT: G9958"

franslation="MOARYSVSDPNALGVVPYLSEQNYYRAAGSYGGMASPMGVYSGH

franslation="MOARYSVSDPNALGVVPYLSEQNYYRAAGSYGGMASPMGVYSGH
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IDR FPFYRENKOGWQNSIRHNLSLNBCFVKVPRDDKKFGKGSYWTLDPDSYNMFENGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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100.0%; Score 986; DB 9; Length 3289;
Best Local Similarity 100.0%; Pred. No. 4.5e-169;
Matches 986; Conservative 0; Mismatches 0; Indels 0
                                                                                                                      2 (bases 1 to 3289)
Miuza,N.
Direct Submission
Submitted (18-SEP-1996) N. Miuza, Akit
Medicine, Department of Biochemistry,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                1 :3289

Coganism="Homo sapiens"

Muol type="genomic DNA"

AD xref="taxon:9606"

1197. 2702

/gene="MFH-1"
          structures
Genomics 41 (3), 489-492 (1997)
97312712
9169153
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                              JOURNAL
MEDLINE
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LENGTH;
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US-09-134-000C-1782/C

Sequence 182, Application US/09134000C

Sequence 182, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1998-08-15

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 1782

LENGTH: 381
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     Length 361;
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                                                0; Indels
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Sequence 9538, Application US/09621976
Sequence 9538, Application US/09621976
Settent No. 66390638
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johnas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERBRICE: GENSET. 054FR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NNS: 19335
SOFTWARE: PATENT: Dm.
Query Match 100.0%; Score 12; DB 3; I Best Local Similarity 100.0%; Pred. no. 1.1e+03; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uvery Match
100.0%; Score 12; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.1e+03
Matches 12; Conservative 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 12; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e+03 Matches 12; Conservative 0; Miematches 0
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                                                                                                                                                  112 GGAAGTAAAA 101
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                                                                                                 1 GGAAAGTAAAA 12
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CORGANISM: Homo sapiens
US-09-621-976-9538
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APPLICANT: Chumakov, IIya
APPLICANT: Cohen, Annick
APPLICANT: Cohen, Annick
APPLICANT: Ochen, Annick
APPLICANT: Ochen, Annick
FILE OF INVENTION: BIALDELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE OF INVENTION: BIALDELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE OF INVOLVED: 02.09/671,317
RICHERT FILING DATE: 2000-03-27
PRICR PILING DATE: 2000-03-23
PRICR PILING DATE: 2000-03-24
PRICR PLICATION NUMBER: US 60/126,269
PRICR PLICATION NUMBER: US 60/126,269
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CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

VINNERS OF SEQ ID NOS: 8252

SEQ ID NO 713

FROM THE TITLE OF THE TIT
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100.0%; Score 12; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 1.16+03;
Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paper, Bryan
APPLICANT: Steahling-Hampton, Karen
APPLICANT: Steahling-Hampton, Karen
TITLE OF INVENTION: GENOMIC DELETIONS
GURRENT FILLE OF INVENTION NUMBER: US/09/918,686
CURRENT FILLE OF DEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NO
SEQ IN NO
SEQ ID NO
SEQ IN NO
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Patent No. 6528260
GENERAL INFORMATION:
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Query Match
100.0%; Score 9; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
CURRENT APPLICATION DATA:
FILING DATE:
PRIOR PRICATION NUMBER: US/08/82,028
FILING DATE:
PRIOR PRICATION NUMBER: US 08/040,687
FILING DATE:
APPLICATION NUMBER: US 0.81
FERFENDENCE DOCKET NUMBER: C-37,075C
TELECOMUNICATION INPORMATION:
INFORMATION FOR SEO ID NO: 35:
EBUGHEN FOR EAST OF SEO ID NO: 35:
LENGTH: 2 Date pairs
TYPE: nucleic acid
INFORMATION FOR SEO ID NO: 35:
FERMIDENESS: double
INFORMATION FOR SEO ID NO: 35:
FERMIDENESS: double
INFORMATION FOR SEO ID NO: 35:
FRANDENESS: double
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                                                                                   Sequence 19, Application 78/08512681
Fatern No. 5755976
GENERAL INFORMATION:
APPLICANT: Ocfiner, Perer J.
APPLICANT: Underhill, Perer A.
TITLE OF INVENTION: by Deneturing High Performance Liquid Chromatography and TITLE OF INVENTION: Methode for Comparative Sequencing NUMBERS:
ADDRESSER: Deflinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CORRESPONDENCE: Associates
STREET: Associates
STREET: Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMMETOR FERENS APPLICANT: GENERAL SEPELCANT: GENERAL SEPELCANT: GENERAL SEPELCANT: RIXON, MARK N ARPLICANT: ANDERSON, HI KERR APPLICANT: KAPLAN, DONALD A APPLICANT: SCHOLOW, USPREZE ATTLE OF INVENTION: NOVEL PAMILY OF KICH APPINITY, ITTLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT ITTLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 22;
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100.04; Score 9; DB 1; Length 22;
Best Local Similarity 100.04; Pred. No. 2.8e+No. 3;
Matche S 9; Conservative 0; Midmatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         STATE: CALO AATO
STATE: CALO
COUNTRY: USA
ZIP: 9430A
COMPUTER: READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TAM FC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
COLECTUE TYPE: DNA
CORGINAL SOURCE:

INDIVIDUAL ISOLATE: DY6234 REVERSE PRIMER
US-08-512-681-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTOMEY/AGENT INFORMATION:
NAME: Evans, Susan I.
REGISTRATION NUMBER: 38,443
REPERBINGE/DOCKET WYMBER: 8600-0155
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 bade pairs
ITYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 Application US/08822028
Patent No. 5993813
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STREET: P.O. BOX 1967
CITY: MIDIAND
STAIR: MICHIGAN
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACAAATGIT 9
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                                                                         2-681-19/c
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Title: Perfect score:

Sequence:

OM nucleic

Scoring table:

Searched:

Database:

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Sequence 43641, A Sequence 256264, Sequence 256264, Sequence 25, Appl. Sequence 21, Appl. Sequence 21, Appl. Sequence 21, Appl. Sequence 211, Appl. Sequence 211, Appl. Sequence 351, Appl. Sequence 1366, Appl. Sequence 1367, Appl. Sequence 259, Appl. Sequence 1367, Appl. Sequence 1, Appl. Seque
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2 US-10-424-599-43641

2 US-10-027-632-256263

3 US-10-027-632-256264

4 US-10-027-632-256264

5 US-10-027-632-256264

5 US-10-027-632-256264

5 US-10-087-086-24

5 US-10-087-086-24

5 US-10-087-086-24

5 US-10-087-086-24

5 US-10-087-086-27

6 US-10-082-187-136

4 US-10-092-184-1369

1 US-09-764-647-1369

1 US-10-09-184-1369

1 US-10-09-184-184-184

1 US-10-09-184-184

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 17; Conservative
Sequence 9718, Apple equence 17, Appl. Sequence 10702, Sequence 10003, A Sequence 977, Apple equence 22032, A Sequence 22032, A Sequence 24033, Sequence 24033, Sequence 24033, Sequence 24132, Sequence 64132, Sequence 64133, Sequence 64133
                                                                                                                                                                                                                                                                                                                 March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*

/ cgn2 6/prodata/1/pubpna/USO7 pUBCOMB.seq:*
/ cgn2 6/prodata/1/pubpna/DSO6 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO6 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO6 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO7 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO8 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO8 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO8 PUBCOMB.seq:*
/ cgn2 6/prodata/1/pubpna/USO8 PUBCOMB.seq:*
/ cgn2 6/prodata/1/pubpna/USO9 PUBCOMB.seq:*
/ cgn2 6/prodata/1/pubpna/USO9 NEW PUB.seq:*
/ cgn2 6/prodata/1/pubpna/USO0 PUBCOMB.seq:*
                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2458946 seqs, 1861504846 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-963-285-1_COPY_359_375
17
1 tgtggaaggaataaata 17
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Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Query
Match Length DB
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6458
493
2523
21619
21619
21619
359
493
589
589
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1 TGTGGAAGGAATAATA 17

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Score

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Sequence 82796, Application US/10424599

Sequence 82796, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ase

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ase

TITLE OF INVENTION: Soy Nucleic Acid Molecules Ase

TITLE OF INVENTION: Soy Nucleic Acid Molecules Acid Mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10003. Application US/09764891;
publication No. USZ0030077808A1
| GENERAL INFORMATION:
| APPLICANT: ROGEN et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| FILZ PERENCE.
| CURRENT APPLICATION UNHER: US/09/764,891 |
| CURRENT APPLICATION UNHER: US/09/764,891 |
| PRIOR APPLICATION GAIS = E001-01-17 |
| PRIOR APPLICATION GAIS = E001-01-17 |
| PRIOR APPLICATION GAIS = E001-01-17 |
| PRIOR APPLICATION OF = E001-01-17 |
| SEQ ID NO: 1003 |
| LENGTH: 11619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2523;
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94.1%; Score 16; DB 12; Length 25

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE INFORMATION: Clone ID: PAT_MRT3847_45782C.1 US-10-44-599-82796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 GTGGAAGGAATAAATA 617
                                                                                                                                                 233 GTGGAAGGAATAATA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GTGGAAGGAATAATA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-764-891-10003/C
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Publication No. US20040031072A1
Publication No. US20040031072A1
Publication No. US20040031072A1
Publication No. US20040031072A1
Publication No. US2004003107A1
APPLICANT: Knowlic David K
APPLICANT: Cac Yongwei
APPLICANT: Cac Yongwei
APPLICANT: Cac Yongwei
APPLICANT: Cac Yongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US 10.424.599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DAILS
TOTAL SOO ID NOS: 285684
EIENGTH: 493
PUBLICATION NOS: 285684
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                                                                                                                                                                                                                                                                                            US-US-Y85-285-1
Sequence 1, Application US/05963285
FRACENT NO. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Enchock, Sven
APPLICANT: Excok, Katarina
APPLICANT: ROOK, Katarina
APPLICANT: ROOK, Katarina
APPLICANT: RONGHI, Lene
TILLE OF INVENTION: PROMOTER EQUENCES
FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: SE 0004102-0
FRIOR APPLICATION NUMBER: SE 0004102-0
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-09-26
NUMBER OF FRIOR DATE: 2000-09-26
NUMBER OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 TGTGGAAGGAATAAATA 375
1 TGTGGAAGGAATAAATA 17
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MAME/KEY: CDS

LOCATION: (2235)...(3737)

US-09-963-285-1
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US-10-205-428-977/c
; Sequence 977, Application US/10205428
; Sequence 977, Application US/10205428
; CENERLI INFORMATION:
; APPLICANT: Rosen et 7
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                         Query Match
94.1%; Score 16; DB 10; L
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                 5310 TGTGGAAGGAATAAT 5295
                                                                                                                                                                                                                                1 TGTGGAAGGAATAAT 16
TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-891-10003
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Query Match

94.1%; Score 16; DB 12; Length 493;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels

FEATURE:
NAMB/KES;
NAMB/KES;
LOCATION: (1)..(493)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68271C.1
US-10-424-599-107702

TYPE: DNA ORGANISM: Glycine max

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